

ABSTRACT OF THE DISCLOSURE

Methods are disclosed for predicting the potential of an oligonucleotide to hybridize to a target nucleotide sequence. A predetermined number of unique oligonucleotides is identified. The unique oligonucleotides are chosen to sample the entire length of a nucleotide sequence that is hybridizable with the target nucleotide sequence. At least one parameter that is independently predictive of the ability of each of the oligonucleotides of the set to hybridize to the target nucleotide sequence is determined and evaluated for each of the above oligonucleotides. A subset of oligonucleotides within the predetermined number of unique oligonucleotides is identified based on the evaluation of the parameter. Oligonucleotides in the subset are identified that are clustered along a region of the nucleotide sequence that is hybridizable to the target nucleotide sequence. The method may be carried out with the aid of a computer.

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